POPULATIONS GENETIC DIVERSITY OF *TRICHOGRAMMA PRETIOSUM* RILEY, 1879 (HYMENOPTERA: TRICHOGRAMMATIDAE), BASED ON THE SEQUENCING OF ITS2 REGION OF THE RIBOSOMAL DNA.

Nilene Rodrigues dos Santos[1], Raul Porfírio de Alameida[2], Itácio Q. M. Padilha[1], Demetrius Antônio M. de Araújo[1], Antônio J. Creão Duarte[1]

[1] UFPB- Universidade Federal da Paraíba (nileners@yahoo.com.br), [2] Embrapa Algodão

Species of the Trichogramma genus are important biological control agents in agricultural production systems and *Trichogramma pretiosum* is the most frequent species in the South American Continent and is associated with several hosts. In studies of the genetic diversity of populations, molecular markers are an efficient tool to detect DNA polymorphism. There are several techniques available to detect DNA polymorphism among populations, among them, the ribosomal DNA sequencing. This work aimed to estimate the degree of genetic differentiation among the populations of *T. pretiosum* obtained from 11 counties in Brazil. After DNA extraction and standardization, PCR reactions, using specific markers, were performed followed by the sequencing and alignment of the samples, being possible to verify the nucleotide composition, multiple alignments, matrices of genetic distance and multiple clusters among the studied populations. With the query results for similarity using the BLAST program in the GenBank database (NCBI - National Center for Biotechnology Information) in all the studied samples, a maximum identification average of 92,2% was obtained for the *Trichogramma pretiosum* species, confirming the correct sequencing. The size of the sequences ranged from 355 to 503 bp. The average G + C content (guanine + cytosine) was 53,2%. After the alignment of 11 sequences of *T. pretiosum*, 391 sites were found conserved, reflecting 73% of the total of 536 sites found, confirming the similarity between samples, as well as reliability in the sequences obtained. According to the dendrogram obtained from the genetic distance matrix using the neighbor-joining method, the presence of four groups was verified. The first group was formed by the TPAES, TPPARS, TPRMT TPCVMT populations; the second by the TPSPMT population; the third by the TPPPE, TPMVCE, TPPPB, TPPPMT, TPJSP populations; and the fourth by the TPPLMT population, being the most genetically distant population. The geographical distance did not affect the genetic similarity or dissimilarity between parasitoids, without significant difference between the geographic distance and the genetic similarity of the samples of *T. pretiosum* in the collected locations. (Fonte Financiadora: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - CAPES).